# Intramembrane Hairpin Loops – an analysis of interactions between proteins and lipid droplets

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Lipid droplets (LDs) are organelles found in almost all organisms that store energy in the form of neutral lipids, such as triglycerides and cholesteryl esters. Beside this metabolic function, LDs fulfill many different roles, such as lipid transport and metabolism or protein storage and degradation. LDs display a very unique structure, being enclosed only by a monolayer of phospholipids. Due to these unique surface properties, only a limited number of protein interactions have been described: direct interaction through amphipathic helix and hairpin, and indirect interaction through protein-protein interaction and lipoylated modifications. If the sequences of several LD proteins have been described over the last few years, no unifying features have been highlighted and the molecular mechanisms behind the targeting remain mostly unknown. Using molecular dynamics, here we show that charged residues are an important but not necessary feature for LD targeting through hairpins and that distribution of charged lipid around LDs may also influence the binding, also without being a necessary condition, using as a model peptide Lipid droplet assembly factor 1 (LDAF1), a protein recently highlighted for its involvement in LD formation.

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